GRAPHIE: Graph Based Histology Image Explorer

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Introduction

- Histology images comprise one of the important sources of knowledge for phenotyping studies in systems biology.
- However, the annotation and analyses of histological data has remained manual, subjective and low-throughput.

GRAPHIE - A visual analytics tool to explore, annotate and reveal potential relationships in histology image collections within a biologically relevant experimental context.

Image Representation

We choose bag-of-features (BoFs) approach to represent a collection of histology images.

An image set is sampled from the collection, image features are extracted, a visual dictionary is built as a summary of these features.

Each image in the collection is represented by the frequency of the dictionary codewords that it contains.

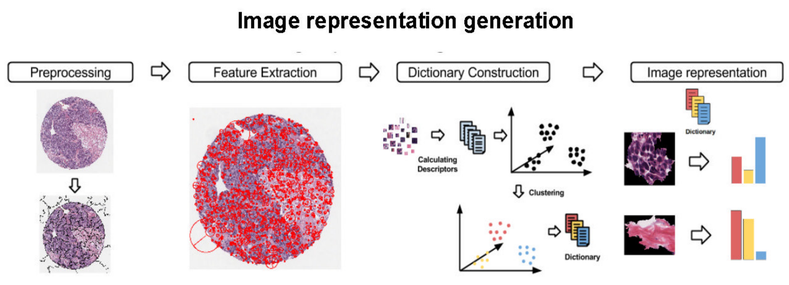

Figure 1. Workflow to create image representations: (a) Preprocess each given histology image. (b) Extract valid feature set. (c) Build a feature dictionary through unsupervised clustering. (d) Generate the bag-of-features image representation

Visualization Components in GRAPHIE

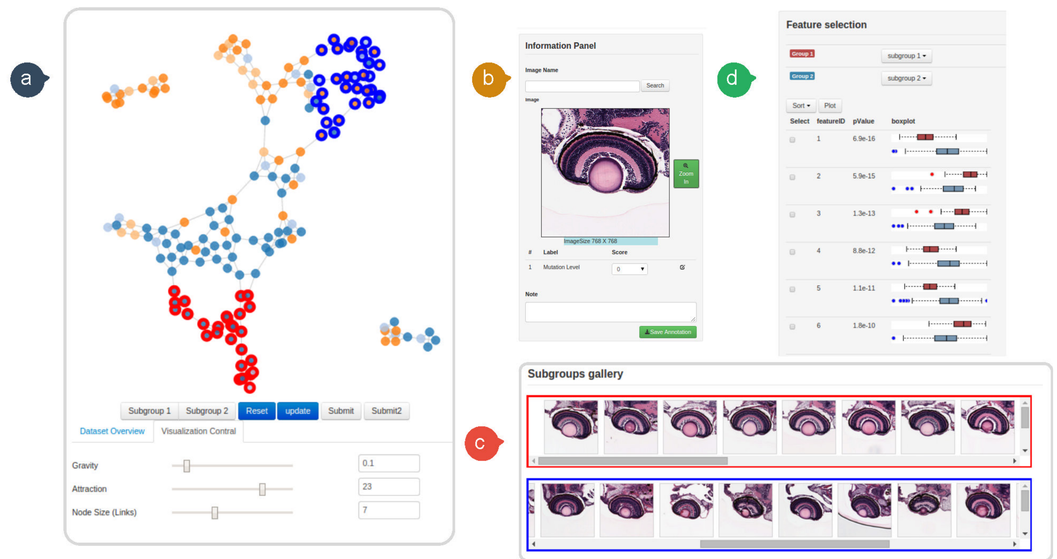

Figure 2. The main GRAPHIE interface: (a) Graph visualization of the image collection. (b) Individual image view. (c) Subgroups gallery. (d) Feature selection view.

(a) Graph visualization of image collection
GRAPHIE adopts the k-nearest neighbour (kNN) graph of a dataset, extract and summarize the topology of the underlying feature space in order to effectively visualize the data.

(b) Individual image view
The individual image view provides detailed information pertaining to individual images and allows users to edit the annotation of selected image.

(c) Subgroups gallery
The subgroups gallery component enables interactively browsing and comparing subgroups when needed

(d) Feature selection view
The feature selection view enables users to examine the distinctiveness of visual words for selected groups of images, therefore enhancing the visualization.

Bibliography

Ding, Hao, et al. “GRAPHIE: graph based histology image explorer.” BMC bioinformatics 16.Suppl 11 (2015): S10.

Case Study

Case study 1. Zebrafish retina histology images

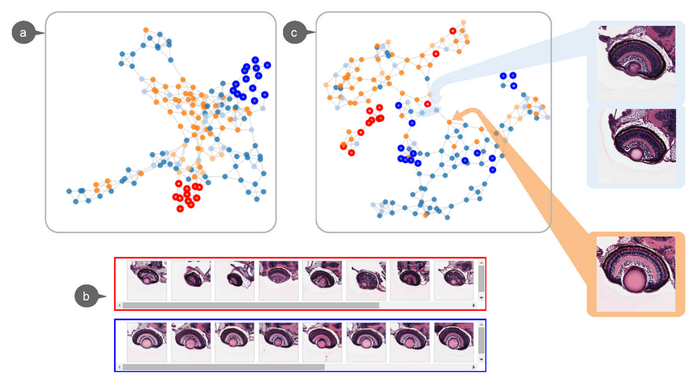

Figure 3. (a)Initial graph visualization. (b) Example phenotypes of the zebrafish retina: (red) retina of a mutant zebrafish. (blue) Eye of wildtype zebrafish. © Graph created with selected features Here, we show three mis-annotated examples, with the upper two images were mis-annotated as wild type and lower image being mis-annotated as mutant.

Case study 2. Epithelial-stromal

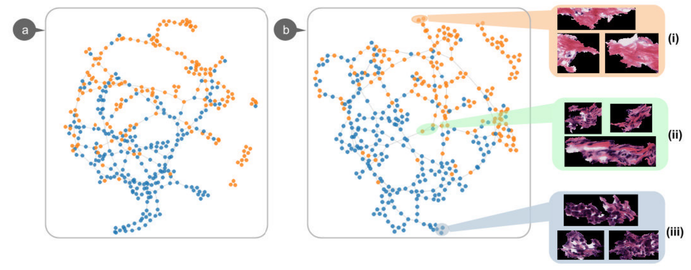

Figure 4. Epithelial-stromal case study. (a) Initial graph visualization. (b) Graph created with selected features. The new graph shows improvement on the separation between the two types of tissue patches. In addition, distinct groups are delineated. For instance, subgroup i (Fig.4(b)) includes purely stromal patches, while subgroup iii includes only epithelium patches. Subgroup ii includes patches with a mixture of stromal and epithelium. This organization of images is very valuable.

Implementation

The data processing is implemented with R script which is triggered by Javascript. The interactive visualization is created using d3.js, a visualization JavaScript library.

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